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APR 18 2001

TECH CENTER 1600/2900

1652

RAW SEQUENCE LISTING

DATE: 04/06/2001

PATENT APPLICATION: US/09/173,463

TIME: 10:50:16

Input Set : A:\429.app.txt

Output Set: N:\CRF3\04062001\I173463.raw

P.S

ENTERED

4 <110> APPLICANT: Black, Margaret E.
6 <120> TITLE OF INVENTION: THYMIDINE KINASE MUTANTS AND FUSION
7 PROTEINS HAVING THYMIDINE KINASE AND GUANYLATE KINASE
8 ACTIVITIES
10 <130> FILE REFERENCE: 240083.429
12 <140> CURRENT APPLICATION NUMBER: US 09/173,463
13 <141> CURRENT FILING DATE: 1998-10-14
15 <160> NUMBER OF SEQ ID NOS: 121
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1131
21 <212> TYPE: DNA
22 <213> ORGANISM: Herpesviridae sp.
24 <400> SEQUENCE: 1
25 atggcttcgt accccggcca tcaacacgcg tctgcgttcg accaggctgc gcgtttctgcg 60
26 ggccatagca accgacgtac ggcgttgccg cctcgccggc agcaagaagc cacggaagtc 120
27 cgcttgagc agaaaatgcc cacgctactg cgggtttata tagacgggcc tcacgggatg 180
28 gggaaaacca ccaccacgca actgctggtg gccctgggtt cgcgcgacga tatcgtctac 240
29 gtacccgagc cgatgactta ctggcagggt ctgggggctt ccgagacaat cgcgaacatc 300
30 tacaccacac aacaccgcct cgaccagggt gagatatcgg ccggggacgc ggcggtggtg 360
31 atgacaagcg ccagataaac aatgggcatg ccttatgcg tgaccgacgc cgttctggtc 420
32 cctcatatcg ggggggaggg tgggagctca catgccccgc ccccgccct caccctcatc 480
33 ttcgaccgcc atcccatcgc cgccctcctg tgctaccggc ccgcgcggtg ccttatgggc 540
34 agcatgaccc ccaggccgt gctggcggtc gtggccctca tccgcgcgac cttgcccggc 600
35 accaaccatg tgcttggggc ccttcgggag gacagacaca tcgaccgcct ggccaaacgc 660
36 cagcgccccg gcgagcggtt ggacctggt atgctgggtg cgattcgccg cgtttacggg 720
37 ctacttgcca atacggtgcg gtatctgcag tgcggcggtt cgtggcggtg ggactgggga 780
38 cagctttcgg ggacggcgt gccgccccag ggtgccgagc ccagagcaa cgcggggcca 840
39 cgaccccata tcggggacac gttatttacc ctgtttcggg ccccgagtt gctggcccc 900
40 aacggcgacc tgtatacgt gtttgctgg gccttggacg tcttggccaa acgcctccgt 960
41 tccatgcacg tctttatcct ggattacgac caatcgccg ccggtgccc ggacgcctg 1020
42 ctgcaactta cctccgggat ggtccagacc cagtcacca ccccggtc cataccgacg 1080
43 atatgcgacc tggcgcgcac gtttgcccg gagatggggg aggctaactg a 1131
45 <210> SEQ ID NO: 2
46 <211> LENGTH: 52
47 <212> TYPE: DNA
48 <213> ORGANISM: Artificial Sequence
50 <220> FEATURE:
51 <223> OTHER INFORMATION: Oligonucleotide for generation of TK mutants
53 <400> SEQUENCE: 2
54 tgggagctca catgccccgc ccccgccct caccctcatc ttcgatcgcc at 52
56 <210> SEQ ID NO: 3
57 <211> LENGTH: 56
58 <212> TYPE: DNA
59 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: Oligonucleotide for generation of TK mutants

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64 <221> NAME/KEY: misc_feature
 65 <222> LOCATION: (1)...(56)
 66 <223> OTHER INFORMATION: n = A,T,C or G
 68 <400> SEQUENCE: 3
 69 atgaggtacc gnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnatggcg atcgaa 56
 71 <210> SEQ ID NO: 4
 72 <211> LENGTH: 17
 73 <212> TYPE: DNA
 74 <213> ORGANISM: Artificial Sequence
 76 <220> FEATURE:
 77 <223> OTHER INFORMATION: Primer
 79 <400> SEQUENCE: 4
 80 cccctccagc gcggtac 17
 82 <210> SEQ ID NO: 5
 83 <211> LENGTH: 17
 84 <212> TYPE: DNA
 85 <213> ORGANISM: Artificial Sequence
 87 <220> FEATURE:
 88 <223> OTHER INFORMATION: Primer
 90 <400> SEQUENCE: 5
 91 cgcgctcgag gggagct 17
 93 <210> SEQ ID NO: 6
 94 <211> LENGTH: 21
 95 <212> TYPE: DNA
 96 <213> ORGANISM: Artificial Sequence
 98 <220> FEATURE:
 99 <223> OTHER INFORMATION: Primer
 101 <400> SEQUENCE: 6
 102 tgggagctca catgccccgc c 21
 104 <210> SEQ ID NO: 7
 105 <211> LENGTH: 11
 106 <212> TYPE: DNA
 107 <213> ORGANISM: Artificial Sequence
 109 <220> FEATURE:
 110 <223> OTHER INFORMATION: Primer
 112 <400> SEQUENCE: 7
 113 atgaggtacc g 11
 115 <210> SEQ ID NO: 8
 116 <211> LENGTH: 52
 117 <212> TYPE: DNA
 118 <213> ORGANISM: Artificial Sequence
 120 <220> FEATURE:
 121 <223> OTHER INFORMATION: Oligonucleotide for generation TK mutants
 123 <400> SEQUENCE: 8
 124 tgggagctca catgccccgc ccccgccct caccctcatc ttcgatcgcc at 52
 126 <210> SEQ ID NO: 9
 127 <211> LENGTH: 70
 128 <212> TYPE: DNA
 129 <213> ORGANISM: Artificial Sequence

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131 <220> FEATURE:
132 <223> OTHER INFORMATION: Oligonucleotide for generation TK mutants
134 <400> SEQUENCE: 9
135 tgggagctca catgccccgc ccccggccct caccctcatc ttcgaccgcc atcccatcgc      60
136 cgccctcctg                                     70
138 <210> SEQ ID NO: 10
139 <211> LENGTH: 38
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Oligonucleotide for generation TK mutants
146 <400> SEQUENCE: 10
147 atgaggtacc gcgcagctgg gtagcacagg agggcggc      38
149 <210> SEQ ID NO: 11
150 <211> LENGTH: 17
151 <212> TYPE: DNA
152 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: Primer
157 <400> SEQUENCE: 11
158 catgccttat gccgtga      17
160 <210> SEQ ID NO: 12
161 <211> LENGTH: 33
162 <212> TYPE: DNA
163 <213> ORGANISM: Herpesviridae sp.
165 <220> FEATURE:
166 <221> NAME/KEY: CDS
167 <222> LOCATION: (1)...(33)
169 <400> SEQUENCE: 12
170 ccc atc gcc gcc ctc ctg tgc tac ccg gcc gcg      33
171 Pro Ile Ala Ala Leu Leu Cys Tyr Pro Ala Ala
172 1          5          10
175 <210> SEQ ID NO: 13
176 <211> LENGTH: 11
177 <212> TYPE: PRT
178 <213> ORGANISM: Herpesviridae sp.
180 <400> SEQUENCE: 13
181 Pro Ile Ala Ala Leu Leu Cys Tyr Pro Ala Ala
182 1          5          10
184 <210> SEQ ID NO: 14
185 <211> LENGTH: 33
186 <212> TYPE: DNA
187 <213> ORGANISM: Artificial Sequence
189 <220> FEATURE:
190 <223> OTHER INFORMATION: HSVTK Mutant
192 <221> NAME/KEY: CDS
193 <222> LOCATION: (1)...(33)
195 <400> SEQUENCE: 14
196 ccc atc gcc tcc ctc ctg tgc tac ccg gcc gcg      33

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```

197 Pro Ile Ala Ser Leu Leu Cys Tyr Pro Ala Ala
198 1 5 10
201 <210> SEQ ID NO: 15
202 <211> LENGTH: 11
203 <212> TYPE: PRT
204 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE:
207 <223> OTHER INFORMATION: HSVTK Mutant
209 <400> SEQUENCE: 15
210 Pro Ile Ala Ser Leu Leu Cys Tyr Pro Ala Ala
211 1 5 10
213 <210> SEQ ID NO: 16
214 <211> LENGTH: 33
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: HSVTK Mutant
221 <221> NAME/KEY: CDS
222 <222> LOCATION: (1)...(33)
224 <400> SEQUENCE: 16
225 tcc atc ggc gcc cta cag tgc tac ccg gtc gcg 33
226 Ser Ile Gly Ala Leu Gln Cys Tyr Pro Val Ala
227 1 5 10
230 <210> SEQ ID NO: 17
231 <211> LENGTH: 11
232 <212> TYPE: PRT
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: HSVTK Mutant
238 <400> SEQUENCE: 17
239 Ser Ile Gly Ala Leu Gln Cys Tyr Pro Val Ala
240 1 5 10
242 <210> SEQ ID NO: 18
243 <211> LENGTH: 33
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: HSVTK Mutant
250 <221> NAME/KEY: CDS
251 <222> LOCATION: (1)...(33)
253 <400> SEQUENCE: 18
254 ccc atc gcc acc ctg ctg tgc tac ccg gcc gcg 33
255 Pro Ile Ala Thr Leu Leu Cys Tyr Pro Ala Ala
256 1 5 10
259 <210> SEQ ID NO: 19
260 <211> LENGTH: 11
261 <212> TYPE: PRT
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:

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```

265 <223> OTHER INFORMATION: HSVTK Mutant
267 <400> SEQUENCE: 19
268 Pro Ile Ala Thr Leu Leu Cys Tyr Pro Ala Ala
269 1 5 10
271 <210> SEQ ID NO: 20
272 <211> LENGTH: 33
273 <212> TYPE: DNA
274 <213> ORGANISM: Artificial Sequence
276 <220> FEATURE:
277 <223> OTHER INFORMATION: HSVTK Mutant
279 <221> NAME/KEY: CDS
280 <222> LOCATION: (1)...(33)
282 <400> SEQUENCE: 20
283 ccc atc gcc gcc tta ctg tta tac ccg acc gcg 33
284 Pro Ile Ala Ala Leu Leu Leu Tyr Pro Thr Ala
285 1 5 10
288 <210> SEQ ID NO: 21
289 <211> LENGTH: 11
290 <212> TYPE: PRT
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: HSVTK Mutant
296 <400> SEQUENCE: 21
297 Pro Ile Ala Ala Leu Leu Leu Tyr Pro Thr Ala
298 1 5 10
300 <210> SEQ ID NO: 22
301 <211> LENGTH: 33
302 <212> TYPE: DNA
303 <213> ORGANISM: Artificial Sequence
305 <220> FEATURE:
306 <223> OTHER INFORMATION: HSVTK Mutant
308 <221> NAME/KEY: CDS
309 <222> LOCATION: (1)...(33)
311 <400> SEQUENCE: 22
312 ccc atc gcc gcc ctc gtg tgc tac ccg gcc gcg 33
313 Pro Ile Ala Ala Leu Val Cys Tyr Pro Ala Ala
314 1 5 10
317 <210> SEQ ID NO: 23
318 <211> LENGTH: 11
319 <212> TYPE: PRT
320 <213> ORGANISM: Artificial Sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: HSVTK Mutant
325 <400> SEQUENCE: 23
326 Pro Ile Ala Ala Leu Val Cys Tyr Pro Ala Ala
327 1 5 10
329 <210> SEQ ID NO: 24
330 <211> LENGTH: 58
331 <212> TYPE: DNA

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:69 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25